



NCBI Conserved Domain Search

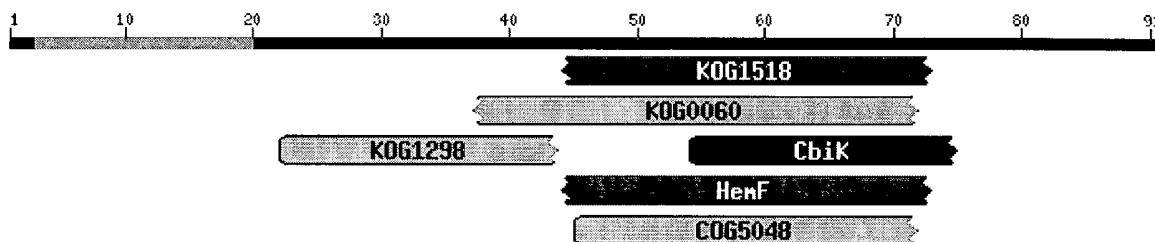
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RPS-BLAST 2.2.6 [Apr-09-2003]

 Query= local sequence:
(91 letters)

 Database: cdd.v1.65
18,039 PSSMs; 5,506,404 total columns

Click on boxes for multiple alignments



Show

Domain Relatives

- .. This CD alignment includes 3D structure. To display structure, download [Cn3D!](#)

PSSMs producing significant alignments:

 Score E
(bits) valu

gnl CDD 19306 KOG1518, KOG1518, Coproporphyrinogen III oxidase CPO/HEM13 [Co...	25.7	1.7
gnl CDD 17858 KOG0060, KOG0060, Long-chain acyl-CoA transporter, ABC superfa...	25.6	2.0
● gnl CDD 13956 COG4822, CbiK, Cobalamin biosynthesis protein CbiK, Co2+ chela...	24.5	4.5
gnl CDD 10282 COG0408, HemF, Coproporphyrinogen III oxidase [Coenzyme metabo...	24.1	6.4
gnl CDD 14178 COG5048, COG5048, FOG: Zn-finger [General function prediction ...	23.6	8.1
gnl CDD 19087 KOG1298, KOG1298, Squalene monooxygenase [Lipid transport and ...	23.7	8.3

[gnl|CDD|19306](#), KOG1518, KOG1518, KOG1518, Coproporphyrinogen III oxidase CPO/HEM13
[Coenzyme transport and metabolism]

CD-Length = 382 residues, only 7.9% aligned
Score = 25.7 bits (56), Expect = 1.7

Query: 44 PLYFSPKCSKHFHRLYHNTRDCTIPAYYKR 73
Sbjct: 214 PSYLFEEDGKHFHQLHKEACDKHDPTFYPR 243

[gnl|CDD|17858](#), KOG0060, KOG0060, KOG0060, Long-chain acyl-CoA transporter, ABC superfamily
(involved in peroxisome organization and biogenesis) [Lipid transport and metabolism, General function

prediction only]

CD-Length = 659 residues, only 5.0% aligned
Score = 25.6 bits (56), Expect = 2.0

Query: 37 FLKHLTGPLY--FSPKCSKHFHRLYHNTRDCTIPAYYK 72
Sbjct: 141 LLKFTTNELYLRFRKNLTKYLHRLYFKGF-----TYYK 173

● gnl|CDD|13956, COG4822, CbiK, Cobalamin biosynthesis protein CbiK, Co²⁺ chelatase [Coenzyme metabolism]

CD-Length = 265 residues, only 8.3% aligned
Score = 24.5 bits (53), Expect = 4.5

Query: 54 HFHRLYHNTRDCTIPAYYKRCA 75
Sbjct: 9 SFGTTYNDTRELTIDAIEEKVA 30

gnl|CDD|10282, COG0408, HemF, Coproporphyrinogen III oxidase [Coenzyme metabolism]

CD-Length = 303 residues, only 9.9% aligned
Score = 24.1 bits (52), Expect = 6.4

Query: 44 PLYFSPKCSKHFHRLYHNTRDCTIPAYYKR 73
Sbjct: 137 PYYGFEEDAVHFHRAAKDACDPHGPEDYPR 166

gnl|CDD|14178, COG5048, COG5048, FOG: Zn-finger [General function prediction only]

CD-Length = 467 residues, only 6.0% aligned
Score = 23.6 bits (49), Expect = 8.1

Query: 45 LYFSPKCSKHFHRLYHNTRDCTIPAYYK 72
Sbjct: 33 PDSCPNC TDSFSRLEHLTRHIRSHTGEK 60

gnl|CDD|19087, KOG1298, KOG1298, KOG1298, Squalene monooxygenase [Lipid transport and metabolism]

CD-Length = 509 residues, only 4.5% aligned
Score = 23.7 bits (51), Expect = 8.3

Query: 22 QRVEIVPRDLRMKDKFLKHLTGP 44
Sbjct: 69 RRVHVIERDLSEPDRIVGELLQP 91

Citing CD-Search: Marchler-Bauer A, Anderson JB, DeWeese-Scott C, Fedorova ND, Geer LY, He S, Hurwitz DI, Jackson JD, Jacobs AR, Lanczycki CJ, Liebert CA, Liu C, Madej T, Marchler GH, Mazumdar R, Nikolskaya AN, Panchenko AR, Rao BS, Shoemaker BA, Simonyan V, Song JS, Thiessen RA,

Vasudevan S, Wang Y, Yamashita RA, Yin JJ, and Bryant SH (2003), "*CDD: a curated Entrez database of conserved domain alignments*", **Nucleic Acids Res.** **31**:383-387.

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results of BLAST

BLASTP 2.2.8 [Jan-05-2004]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1082658391-26650-101718401887.BLASTQ3

Query=

(91 letters)

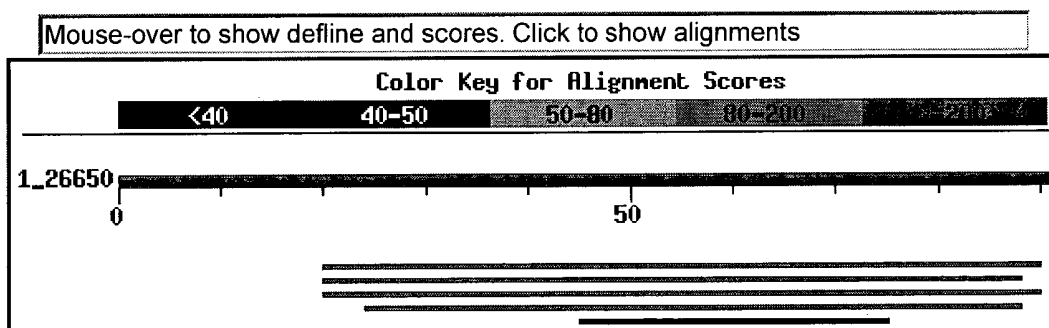
Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF

2,768,312 sequences; 778,115,222 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 5 Blast Hits on the Query Sequence



Sequences producing significant alignments:

	Score	E	
	(bits)	Value	
gi 27479893 ref XP_211736.1 hypothetical protein XP_211736...	140	1e-32	L
gi 28204858 gb AAH46522.1 Unknown (protein for IMAGE:50608...	137	9e-32	
gi 37182157 gb AAQ88881.1 RGP542 [Homo sapiens]	130	1e-29	
gi 41148699 ref XP_372041.1 similar to RPLK9433 [Homo sapi...	104	8e-22	L
gi 16754844 emb CAD10675.2 Mig1 protein [Debaryomyces occi...	31	8.5	

Alignments

☐ >gi|27479893|ref|XP_211736.1| ☒ hypothetical protein XP_211736 [Homo sapiens]
Length = 152

Score = 140 bits (352), Expect = 1e-32
Identities = 71/71 (100%), Positives = 71/71 (100%)

Query: 21 EQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNTRDCTIPAYYKRCARLLTR 80
EQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNTRDCTIPAYYKRCARLLTR
Sbjct: 81 EQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNTRDCTIPAYYKRCARLLTR 140

Query: 81 LAVSPVCMEDK 91
LAVSPVCMEDK
Sbjct: 141 LAVSPVCMEDK 151

☐ >gi|28204858|gb|AAH46522.1| Unknown (protein for IMAGE:5060814) [Mus musculus]
Length = 298

Score = 137 bits (344), Expect = 9e-32
Identities = 68/69 (98%), Positives = 69/69 (100%)

Query: 21 EQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNTRDCTIPAYYKRCARLLTR 80
EQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNTRDCTIPAYYKRCARLLTR
Sbjct: 229 EQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNTRDCTIPAYYKRCARLLTR 288

Query: 81 LAVSPVCME 89
LAVSP+CME
Sbjct: 289 LAVSPMCME 297

☐ >gi|37182157|gb|AAQ88881.1| RGPG542 [Homo sapiens]
Length = 91

Score = 130 bits (326), Expect = 1e-29
Identities = 71/71 (100%), Positives = 71/71 (100%)

Query: 21 EQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNTRDCTIPAYYKRCARLLTR 80
EQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNTRDCTIPAYYKRCARLLTR
Sbjct: 21 EQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNTRDCTIPAYYKRCARLLTR 80

Query: 81 LAVSPVCMEDK 91
LAVSPVCMEDK
Sbjct: 81 LAVSPVCMEDK 91

☐ >gi|41148699|ref|XP_372041.1| ☒ similar to RPLK9433 [Homo sapiens]
gi|37181538|gb|AAQ88580.1| ☒ RPLK9433 [Homo sapiens]
Length = 129

Score = 104 bits (259), Expect = 8e-22
Identities = 49/65 (75%), Positives = 58/65 (89%)

Query: 25 EIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFHRLYHNTRDCTIPAYYKRCARLLTRLAVS 84
EI PRD +KDKF+KH TGP+ FSP+CSKHFHRLY+NTR+C+ PAYYKRCARLLTRLAVS
Sbjct: 64 EIFPRDSNLKDKFIKHFTGPTVTFSPKCSKHFHRLYNTRECSTPAYYKRCARLLTRLAVS 123

Query: 85 PVCME 89
P+C +
Sbjct: 124 PLCSQ 128

☐ >gi|16754844|emb|CAD10675.2| Mig1 protein [Debaryomyces occidentalis]
Length = 458

Score = 31.2 bits (69), Expect = 8.5
Identities = 16/42 (38%), Positives = 19/42 (45%), Gaps = 11/42 (26%)

Query: 46 YFSPKCSKHFHRLYHNTR-----DCTIPAYYKRCAR 76
Y P C K FHRL H TR CT P +K+ +R
Sbjct: 24 YKCPMCGKAFHRLEHQTRHIRTHTGEKPHSCTFPGCFKKFSR 65

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Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF
Posted date: Apr 19, 2004 3:24 AM
Number of letters in database: 778,115,222
Number of sequences in database: 2,768,312

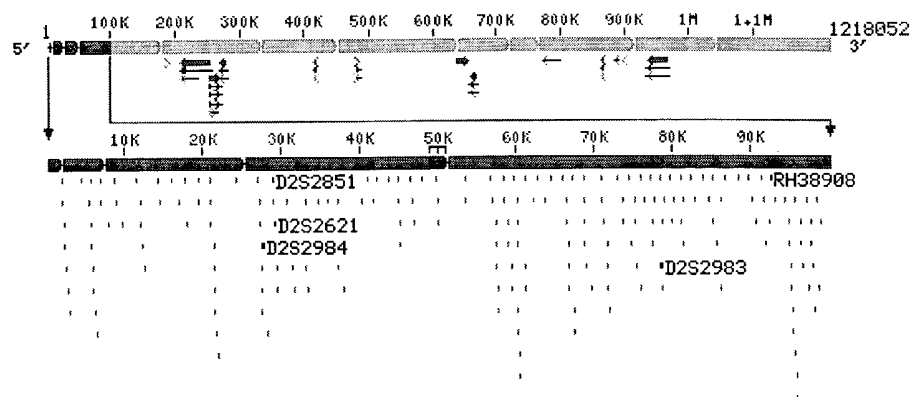
Lambda	K	H
0.330	0.141	0.457

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 10,768,323
Number of Sequences: 2768312
Number of extensions: 339256
Number of successful extensions: 765
Number of sequences better than 10.0: 0
Number of HSP's better than 10.0 without gapping: 0
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 765
Number of HSP's gapped (non-prelim): 0
length of query: 91
length of database: 778,115,222
effective HSP length: 59
effective length of query: 32
effective length of database: 614,784,814
effective search space: 19673114048
effective search space used: 19673114048

T: 11
A: 40
X1: 15 (7.1 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 40 (21.8 bits)
S2: 69 (31.2 bits)

**Legend:**

■ - segment boundaries ■ - region/SNP ■ - other feature
— - sequence fragment shown

Sequence:

49001 TATTATTGGG TAGAAGAGC ATTTGGCTTA GTCATCAAAA GTATAAATC AAGTTTAA
49061 AGCAGCACAA ATGAGCAGAA CTGTGCCTTG GTACCTGTAC GTGAATTTGT GCACAAATG
49121 TTCTTGTGAT TTTCTTGGTT GCCAGAGTAA TGCCAGGCAC CTTGAGGCAC ACAAAGAGG
49181 CATGGCTTCA GGAAGGAGC ATTATTTTCC ATACCATACT GTAGCTGGGC CTTTCTGTA
49241 AACACAGGGG CCACTAGTCT CAGGTCCCAT ATGTGCAGGC CTTCTTTGCC TTTCAGGATA
49301 ATCCAGACAT TTGCTCTGTG TGCAGGATTG ATTCACCCCT CTTAGCACCC ATCTCAGGAG
49361 AGGTCAACAG GGAATATTCC AGGGAATAG GGAAGCAAC CCCAGAGGTA CCTCCAGCCA
49421 GTGAATTGAC TCCCTCCATT CCTCTCTATC TAAGTTCTCT TGCAACTCA CTTCCACCTA
49481 GGAATCCTCA GATTAGGCAG GTCCCACTCT CACTCCTGCC CCTACACAG ATGCCTGGTG
49541 AATATGCCCC CATTAAGTC CAGGTCTTCT TTTCTTTACA GGACTTAAGC CAATTAAAA
49601 GGGATTTTGG CAGTTTTC AAGAGCCCTG ACATGTATAT AGAGGCTTTC CAGAACATA
49661 CCCAGTATT TGAGCTCTCC TAGAAGATG TCAGGTTCTT TTTGAATCAA ACCCTCACCA
dbSNP: 7421233
49721 CTCCTGAAAA GCAGGACACC CTGTAAGTGG CAGACATTTT TGAGGATGAG CTTTATATCT
49781 CATATAGGGC CAGGAGAGAG AAGGAGCCTT ATCCATTGCG AATAATAGCA GTACCATTTG
49841 AAGACCCTAA AAGGAGCCCC AAGATGAAA TGGACCATG AAGCAGGAAA TATTTACGCT
49901 CTGAAGAGGC AACACCCCAA AGATTCTGTA AACTATCCAC AAGAACACTA TGGGGAAGT
49961 GGGGGCTGTA TTCAATTATC TCCACTTGAC CCTGCCCTTA ACATGTGGGG ATTATTACAA
dbSNP: 10195466 dbSNP: 4075373
50021 TTCAGGCTGA GATTTCTATG GGTGGCACT CAGCCCAACC ATATCACCAT GGACCCATA
50081 GTTCCTGCAA TTCTTATACC CTGGGGCCCA GGTGATACCC TTCCACATC TACCTGAGG
50141 GCTGCATGTG CACCACAGCA GCTGGATCTA GCACCGCAGC TGTGACCTCG GCACCCAGC
50201 TCACACATTG CCCTGCATCT CAGGACACAG GTGCTTCAGC ACAGCAGGGA GGCTGACCC
50261 AGGACAGAGC GAGCCACCAT CATGTTTCC CATGGCTCG GAGCCACCTG CTCAGGCTT
50321 GTGCTGCCCC TGCTGGTGCC CTTGCTCCTC CAGTGCAGGA CTGCCACGTG CTCACCTGCA
50381 CCATGAGAGG ACCCAGGAC TGCTGCTCG TGCTGCTGCA CCACCCCTAC CAGTGACTCT
50441 GTCCCTTCTA GTGCTGGAGC CATCATGCAT CCATACATGA TGCCCAAGAG CTCAGAGACC
50501 AGCCTGCCTG GAATCCCTGT CCCCAGCAA GCCATGCCAT AGCTCCCAA AACACCCCA
50561 ACTTAGGCA CTGAGACACT CACAGACACT GCTGATGTTG ATTACATCAA AATAATCAT
50621 ACACAGACTA CATGACTGTG TCCACCCAGA ACCAAGCCA AGCACCATA ATCACTGAC
50681 TCCAGAGGAT ACATCTACAG GAAATGTCT TTCCGTACGA AATATACTTC TTAGATTGG
50741 AAAAGCAAC TCTTCCATCA GATGCACAGA ATCAACATA GGGATCGAGC AACATGGAA
50801 AAGCAAGAA ACGTGACATC TTCAAAGAA CACATAGTT ATCTAGCAC AGCCACAA
50861 GTAAGGAAA GCCATGAAT GCCTGAAAA TATTTCAAAA TAATGATCTT AAGGACTC
50921 AGTGAGATGC AGGAGGCAA AGACAGCAA TTCAGGAAA CAATTCAGC AAATAAAT
50981 CAGGAACA ATTTATAATC T

Font: Line length: Sequence fragment size:

Comments and suggestions to: [\[info@ncbi.nlm.nih.gov\]](mailto:info@ncbi.nlm.nih.gov)



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RPS-BLAST 2.2.6 [Apr-09-2003]

Query= local sequence:
(91 letters)

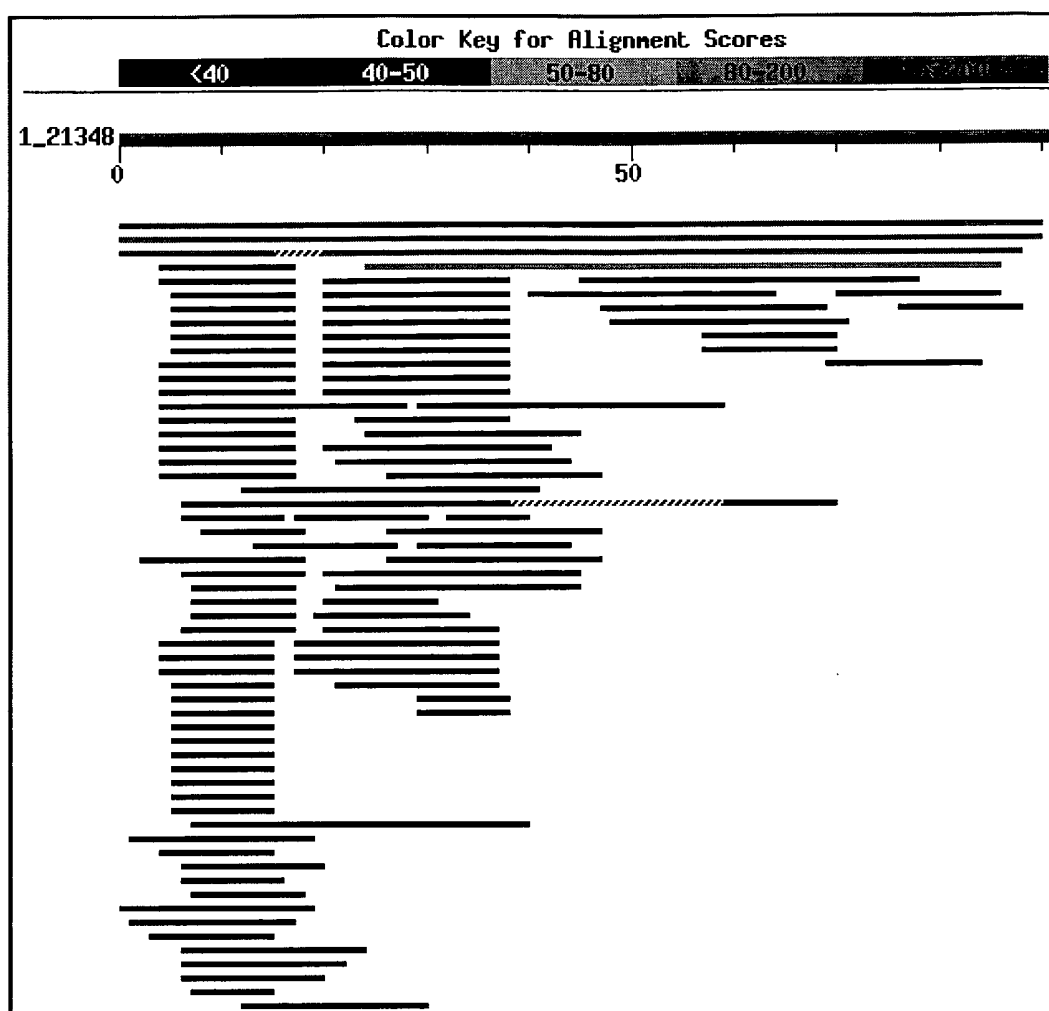
Database: cdd.v1.65
18,039 PSSMs; 5,506,404 total columns

No hits found ..

**...No hits found!**

Citing CD-Search: Marchler-Bauer A, Anderson JB, DeWeese-Scott C, Fedorova ND, Geer LY, He S, Hurwitz DI, Jackson JD, Jacobs AR, Lanczycki CJ, Liebert CA, Liu C, Madej T, Marchler GH, Mazumder R, Nikolskaya AN, Panchenko AR, Rao BS, Shoemaker BA, Simonyan V, Song JS, Thiessen RA, Vasudevan S, Wang Y, Yamashita RA, Yin JJ, and Bryant SH (2003), "*CDD: a curated Entrez database of conserved domain alignments*", **Nucleic Acids Res.** 31:383-387.

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Sequences producing significant alignments:		Score (bits)	E Value
gi 37182157 gb AAQ88881.1	RGPG542 [Homo sapiens]	302	3e-81
gi 27479893 ref XP_211736.1	hypothetical protein XP_211736...	261	6e-69
gi 28204858 gb AAH46522.1	Unknown (protein for IMAGE:50608...	230	1e-59
gi 41148699 ref XP_372041.1	similar to RPLK9433 [Homo sapi...	148	7e-35
gi 6456546 gb AAF09175.1	UDP-glucuronosyltransferase 1A1 [...	37	0.28
gi 6456548 gb AAF09176.1	UDP-glucuronosyltransferase 1A1 [...	37	0.28
gi 31235852 ref XP_319311.1	ENSANGP00000022605 [Anopheles ...	35	0.92
gi 31235881 ref XP_319315.1	ENSANGP00000024583 [Anopheles ...	35	0.92
gi 31235868 ref XP_319313.1	ENSANGP00000023782 [Anopheles ...	35	0.92
gi 31235885 ref XP_319316.1	ENSANGP00000023510 [Anopheles ...	35	0.92
gi 31235859 ref XP_319312.1	ENSANGP00000025304 [Anopheles ...	35	0.92
gi 31235848 ref XP_319310.1	ENSANGP00000024621 [Anopheles ...	35	0.92
gi 31235836 ref XP_319308.1	ENSANGP00000012555 [Anopheles ...	35	0.92
gi 31235874 ref XP_319314.1	ENSANGP00000022367 [Anopheles ...	35	0.92
gi 31235842 ref XP_319309.1	ENSANGP00000024129 [Anopheles ...	35	0.92
gi 6456554 gb AAF09179.1	UDP-glucuronosyltransferase 1A1 [...	35	1.7
gi 13641265 gb AAK31597.1	UDP-glucuronosyltransferase UGT1...	35	1.7
gi 6537144 gb AAF15549.1	UDP-glucuronosyltransferase UGT1A...	35	1.7
gi 13936939 gb AAK49991.1	UDP-glucuronosyltransferase UGT1...	35	1.7
gi 6456556 gb AAF09180.1	UDP-glucuronosyltransferase 1A1 [...	35	1.7

gi 39998404 ref NP_954355.1	major facilitator family trans...	33	4.0	
gi 13569709 gb AAK31204.1	bilirubin UDP-glucuronosyltrasfer...	32	7.2	
gi 8850236 ref NP_000454.1	UDP glycosyltransferase 1 famil...	32	7.2	L
gi 45199011 ref NP_986040.1	AFR493Cp [Eremothecium gossypi...	32	7.2	
gi 3059177 dbj BAA25600.1	bilirubin UDP-glucuronosyltransf...	32	7.2	
gi 6456550 gb AAF09177.1	UDP-glucuronosyltransferase 1A1 [...]	32	7.2	
gi 38106605 gb EAA52893.1	hypothetical protein MG06021.4 [...]	32	7.2	
gi 6010650 gb AAF01205.1	bilirubin UDP-glucuronosyltransfe...	32	7.2	
gi 340132 gb AAA61248.1	bilirubin UDP-glucuronosyltransferase	32	7.2	
gi 12002135 gb AAG43197.1	UDP-glucuronosyltransferase [Hom...	32	7.2	
gi 6456542 gb AAF09173.1	UDP-glucuronosyltransferase 1A1 [...]	32	7.2	
gi 15616196 ref NP_244501.1	transcriptional regulator (Ara...	32	9.7	
gi 179419 gb AAA51822.1	beta-galactosidase precursor (EC 3...	32	13	L
gi 39936770 ref NP_949046.1	Globin-like protein [Rhodopseu...	32	13	
gi 17367360 sp Q63376 NX2B RAT	Neurexin 2-beta precursor (N...	32	13	L
gi 44240564 gb EAH88833.1	unknown [environmental sequence]	32	13	
gi 38099400 gb EAA46751.1	hypothetical protein MG10445.4 [...]	32	13	
gi 23063144 ref ZP_00087886.1	hypothetical protein [Pseudo...	32	13	
gi 19745439 ref NP_606575.1	putative ABC transporter (perm...	31	17	
gi 15674485 ref NP_268659.1	putative ABC transporter (perm...	31	17	
gi 21909771 ref NP_664039.1	putative ABC transporter (perm...	31	17	
gi 34328319 ref NP_083633.2	RIKEN cDNA 2010005A06 [Mus mus...	31	17	L
gi 19115312 ref NP_594400.1	hypothetical protein [Schizosa...	31	17	
gi 21673770 ref NP_661835.1	FecCD transport family protein...	31	17	
gi 43365047 gb EAD47320.1	unknown [environmental sequence]	31	17	
gi 43572144 gb EAE40890.1	unknown [environmental sequence]	31	17	
gi 46362507 gb AAH66572.1	Unknown (protein for IMAGE:68056...	31	23	
gi 40645690 dbj BAD06359.1	putative integral membrane prot...	31	23	
gi 29830792 ref NP_825426.1	putative integral membrane pro...	31	23	
gi 6456552 gb AAF09178.1	UDP-glucuronosyltransferase 1A1 [...]	31	23	
gi 21222362 ref NP_628141.1	possible integral membrane pro...	31	23	
gi 6806893 ref NP_000586.2	lymphotoxin alpha precursor; ly...	30	31	L
gi 31880296 gb AAP51424.1	lymphotoxin alpha precursor [Hom...	30	31	
gi 11875697 gb AAG40760.1	urokinase plasminogen activator ...	30	31	
gi 37527109 ref NP_930453.1	hypothetical protein [Photorha...	30	31	
gi 29247065 gb EAA38639.1	GLP_59_9627_8422 [Giardia lambl...	30	31	
gi 31880292 gb AAP51422.1	lymphotoxin alpha precursor [Hom...	30	31	
gi 31880318 gb AAP51435.1	lymphotoxin alpha precursor [Hom...	30	31	
gi 31880294 gb AAP51423.1	lymphotoxin alpha precursor [Hom...	30	31	
gi 339743 gb AAB59455.1	tumor necrosis factor-beta	30	31	L
gi 31880290 gb AAP51421.1	lymphotoxin alpha precursor [Hom...	30	31	
gi 46107834 ref XP_380976.1	hypothetical protein FG00800.1...	30	31	
gi 356345 prf 1209233A	lymphotoxin	30	31	
gi 37213 emb CAA78746.1	lymphotoxin, Tnfb [Homo sapiens] >...	30	31	L
gi 2493675 sp Q28042 OGP BOVIN	OVIDUCT-SPECIFIC GLYCOPROTEI...	30	31	L
gi 11875701 gb AAG40762.1	urokinase plasminogen activator ...	30	31	
gi 43904856 gb EAG06890.1	unknown [environmental sequence]	30	31	
gi 11875699 gb AAG40761.1	urokinase plasminogen activator ...	30	31	
gi 219914 dbj BAA00064.1	lymphotoxin [Homo sapiens] >gi 31...	30	31	L
gi 34499061 ref NP_903276.1	conserved hypothetical protein...	30	42	
gi 7503491 pir T22238	hypothetical protein F45G2.6 - Caeno...	30	42	
gi 44316755 gb EAI41271.1	unknown [environmental sequence]	30	42	
gi 32565349 ref NP_499773.2	TNF Receptor associated Factor...	30	42	L
gi 39586579 emb CAE73706.1	Hypothetical protein CBG21219 [...]	30	42	
gi 11138413 gb AAG31358.1	dipeptidyl carboxy peptidase 1 [...]	30	42	
gi 29249818 gb EAA41322.1	GLP_163_36481_38211 [Giardia lam...	30	42	
gi 44348846 gb EAI63835.1	unknown [environmental sequence]	30	42	

gi 46366359 ref ZP_00228687.1 	COG1173: ABC-type dipeptide/...	30	42	
gi 43375113 gb EAD52424.1 	unknown [environmental sequence]	30	42	
gi 19552109 ref NP_600111.1 	putative acetyltransferase [Co...	29	57	
gi 15612782 ref NP_241085.1 	L-lactate permease [Bacillus h...	29	57	
gi 16754844 emb CAD10675.2 	Mig1 protein [Debaryomyces occi...	29	57	
gi 26106036 dbj BAC41711.1 	poliovirus receptor [Cebus apella]	29	57	
gi 27381266 ref NP_772795.1 	ABC transporter ATP-binding pr...	29	57	
gi 6475037 dbj BAA87329.1 	sushi-repeat-containing protein ...	29	57	L
gi 41199583 ref XP_372161.1 	similar to CDNA sequence BC004...	29	57	L
gi 34558352 ref NP_908167.1 	hypothetical protein WS2068 [W...	29	57	
gi 23102087 ref ZP_00088614.1 	COG2998: ABC-type tungstate ...	29	57	
gi 37520203 ref NP_923580.1 	two-component hybrid sensor an...	29	57	
gi 16209647 gb AAL14384.1 	AT3g52500/F2206_120 [Arabidopsis...	29	57	
gi 23063253 ref ZP_00087995.1 	COG2822: Predicted periplasm...	29	57	
gi 4758686 ref NP_002323.1 	low density lipoprotein-related...	29	57	L
gi 45547567 ref ZP_00187613.1 	COG1038: Pyruvate carboxylas...	29	57	
gi 42408797 dbj BAD10058.1 	putative aminoacylase [Oryza sa...	29	57	
gi 44609104 gb EAK45181.1 	unknown [environmental sequence]	29	57	
gi 21245005 ref NP_644587.1 	phytochrome-like protein [Xant...	29	57	
gi 845468 gb AAA67825.1 	precursor protein [Hepatitis C vir...	29	57	
gi 46130328 ref ZP_00165149.2 	COG0388: Predicted amidohydr...	29	57	
gi 21323650 dbj BAB98277.1 	Acetyltransferases, including N...	29	57	
gi 34540006 ref NP_904485.1 	hydrolase, carbon-nitrogen fam...	29	57	

Alignments

Get selected sequences

Select all

Deselect all

☐ >[gi|37182157|gb|AAQ88881.1|](#) RGP542 [Homo sapiens]
Length = 91

Score = 302 bits (706), Expect = 3e-81
Identities = 91/91 (100%), Positives = 91/91 (100%)

Query: 1 MRGPGHPLLGLLLVLGPSPEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFRHLYH 60
MRGPGHPLLGLLLVLGPSPEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFRHLYH
Sbjct: 1 MRGPGHPLLGLLLVLGPSPEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFRHLYH 60

Query: 61 NTRDCTIPAYYKRCARLLTRLAVSPVCMEDK 91
NTRDCTIPAYYKRCARLLTRLAVSPVCMEDK
Sbjct: 61 NTRDCTIPAYYKRCARLLTRLAVSPVCMEDK 91

☐ >[gi|27479893|ref|XP_211736.1|](#) **L** hypothetical protein XP_211736 [Homo sapiens]
Length = 152

Score = 261 bits (610), Expect = 6e-69
Identities = 91/151 (60%), Positives = 91/151 (60%), Gaps = 60/151 (39%)

Query: 1 MRGPGHPLL-----LG-----LL-----LV----- 15
MRGPGHPLL LG LL LV
Sbjct: 1 MRGPGHPLLGLLLVLGAAGRGRGAEPREPADGQALLRLVVELVQELRKHHSAEHKGLQ 60
Query: 16 -----LGPSPEQRVEIVPRDLRMKDKFLKHLTGPLYFSPKCSKHFRHLYH 60

4/22/04

Sbjct: 8 GHPLVLGLLLCVLGP 22

☐ >gi|6456548|gb|AAF09176.1| UDP-glucuronosyltransferase 1A1 [Gorilla gorilla]
Length = 29

Score = 37.1 bits (80), Expect = 0.28

Identities = 13/15 (86%), Positives = 14/15 (93%), Gaps = 1/15 (6%)

Query: 5 GHPLLLGLLL-VLGP 18

GHPL+LGLLL VLGP

Sbjct: 8 GHPLVLGLLLCVLGP 22

☐ >gi|31235852|ref|XP_319311.1| ENSANGP00000022605 [Anopheles gambiae]
gi|30174786|gb|EAA43612.1| ENSANGP00000022605 [Anopheles gambiae str. PEST]
Length = 1938

Score = 35.4 bits (76), Expect = 0.92

Identities = 13/21 (61%), Positives = 15/21 (71%), Gaps = 5/21 (23%)

Query: 21 EQRV--EIVPRDLRMKD KFLK 39

EQRV EIV R+LR K+LK

Sbjct: 806 EQRVSLEIVQRNLR---KYLK 823

☐ >gi|31235881|ref|XP_319315.1| ENSANGP00000024583 [Anopheles gambiae]
gi|30174793|gb|EAA43618.1| ENSANGP00000024583 [Anopheles gambiae str. PEST]
Length = 1451

Score = 35.4 bits (76), Expect = 0.92

Identities = 13/21 (61%), Positives = 15/21 (71%), Gaps = 5/21 (23%)

Query: 21 EQRV--EIVPRDLRMKD KFLK 39

EQRV EIV R+LR K+LK

Sbjct: 314 EQRVSLEIVQRNLR---KYLK 331

☐ >gi|31235868|ref|XP_319313.1| ENSANGP00000023782 [Anopheles gambiae]
gi|30174788|gb|EAA43614.1| ENSANGP00000023782 [Anopheles gambiae str. PEST]
Length = 1739

Score = 35.4 bits (76), Expect = 0.92

Identities = 13/21 (61%), Positives = 15/21 (71%), Gaps = 5/21 (23%)

Query: 21 EQRV--EIVPRDLRMKD KFLK 39


EQRV EIV R+LR K+LK

Sbjct: 602 EQRVSLEIVQRNLR---KYLK 619

☐ >gi|31235885|ref|XP_319316.1| ENSANGP00000023510 [Anopheles gambiae]
gi|30174790|gb|EAA43616.1| ENSANGP00000023510 [Anopheles gambiae str. PEST]
Length = 1315


Score = 35.4 bits (76), Expect = 0.92
Identities = 13/21 (61%), Positives = 15/21 (71%), Gaps = 5/21 (23%)

Query: 21 EQRV--EIVPRDLRMKDKFLK 39
EQRV EIV R+LR K+LK
Sbjct: 152 EQRVSLEIVQRNLR---KYLK 169

 >[gi|31235859|ref|XP_319312.1|](#) ENSANGP00000025304 [Anopheles gambiae]
[gi|30174794|gb|EAA43619.1|](#) ENSANGP00000025304 [Anopheles gambiae str. PEST]
Length = 1938


Score = 35.4 bits (76), Expect = 0.92
Identities = 13/21 (61%), Positives = 15/21 (71%), Gaps = 5/21 (23%)

Query: 21 EQRV--EIVPRDLRMKDKFLK 39
EQRV EIV R+LR K+LK
Sbjct: 806 EQRVSLEIVQRNLR---KYLK 823

 >[gi|31235848|ref|XP_319310.1|](#) ENSANGP00000024621 [Anopheles gambiae]
[gi|30174789|gb|EAA43615.1|](#) ENSANGP00000024621 [Anopheles gambiae str. PEST]
Length = 1937


Score = 35.4 bits (76), Expect = 0.92
Identities = 13/21 (61%), Positives = 15/21 (71%), Gaps = 5/21 (23%)

Query: 21 EQRV--EIVPRDLRMKDKFLK 39
EQRV EIV R+LR K+LK
Sbjct: 806 EQRVSLEIVQRNLR---KYLK 823

 >[gi|31235836|ref|XP_319308.1|](#) ENSANGP00000012555 [Anopheles gambiae]
[gi|30174792|gb|EAA13871.2|](#) ENSANGP00000012555 [Anopheles gambiae str. PEST]
Length = 1943

Score = 35.4 bits (76), Expect = 0.92
Identities = 13/21 (61%), Positives = 15/21 (71%), Gaps = 5/21 (23%)

Query: 21 EQRV--EIVPRDLRMKDKFLK 39
EQRV EIV R+LR K+LK
Sbjct: 806 EQRVSLEIVQRNLR---KYLK 823

 >[gi|31235874|ref|XP_319314.1|](#) ENSANGP00000022367 [Anopheles gambiae]
[gi|30174791|gb|EAA43617.1|](#) ENSANGP00000022367 [Anopheles gambiae str. PEST]
Length = 1644

Score = 35.4 bits (76), Expect = 0.92
Identities = 13/21 (61%), Positives = 15/21 (71%), Gaps = 5/21 (23%)

Query: 21 EQRV--EIVPRDLRMKDKFLK 39
EQRV EIV R+LR K+LK
Sbjct: 507 EQRVSLEIVQRNLR---KYLK 524

☐ >gi|31235842|ref|XP_319309.1| ENSANGP00000024129 [Anopheles gambiae]
gi|30174787|gb|EAA43613.1| ENSANGP00000024129 [Anopheles gambiae str. PEST]
Length = 1937

Score = 35.4 bits (76), Expect = 0.92
Identities = 13/21 (61%), Positives = 15/21 (71%), Gaps = 5/21 (23%)

Query: 21 EQRV--EIVPRDLRMKDKFLK 39
EQRV EIV R+LR K+LK
Sbjct: 806 EQRVSLEIVQRNLR---KYLK 823

☐ >gi|6456554|gb|AAF09179.1| UDP-glucuronosyltransferase 1A1 [Papio cynocephalus]
Length = 28

Score = 34.6 bits (74), Expect = 1.7
Identities = 12/14 (85%), Positives = 13/14 (92%), Gaps = 1/14 (7%)

Query: 6 HPLLLGLLL-VLGP 18
HPL+LGLLL VLGP
Sbjct: 9 HPLVLGLLLCVLGP 22

☐ >gi|13641265|gb|AAK31597.1| UDP-glucuronosyltransferase UGT1A01 [Macaca mulatta]
Length = 533

Score = 34.6 bits (74), Expect = 1.7
Identities = 12/14 (85%), Positives = 13/14 (92%), Gaps = 1/14 (7%)

Query: 6 HPLLLGLLL-VLGP 18
HPL+LGLLL VLGP
Sbjct: 9 HPLVLGLLLCVLGP 22

☐ >gi|6537144|gb|AAF15549.1| UDP-glucuronosyltransferase UGT1A01 [Macaca fascicula]
Length = 533

Score = 34.6 bits (74), Expect = 1.7
Identities = 12/14 (85%), Positives = 13/14 (92%), Gaps = 1/14 (7%)

Query: 6 HPLLLGLLL-VLGP 18
HPL+LGLLL VLGP
Sbjct: 9 HPLVLGLLLCVLGP 22

☐ >gi|13936939|gb|AAK49991.1| UDP-glucuronosyltransferase UGT1A01 [Macaca mulatta]
Length = 533

Score = 34.6 bits (74), Expect = 1.7
Identities = 12/14 (85%), Positives = 13/14 (92%), Gaps = 1/14 (7%)

Query: 6 HPLLLGLLL-VLGP 18
 HPL+LGLLL VLGP
 Sbjct: 9 HPLVLGLLLCVLGP 22

☐ >[gi|6456556|gb|AAF09180.1|](#) UDP-glucuronosyltransferase 1A1 [Colobus guereza]
 Length = 28

Score = 34.6 bits (74), Expect = 1.7
 Identities = 12/14 (85%), Positives = 13/14 (92%), Gaps = 1/14 (7%)

Query: 6 HPLLLGLLL-VLGP 18
 HPL+LGLLL VLGP
 Sbjct: 9 HPLVLGLLLCVLGP 22

☐ >[gi|39998404|ref|NP_954355.1|](#) major facilitator family transporter [Geobacter su
[gi|39985351|gb|AAR36705.1|](#) major facilitator family transporter [Geobacter sulfur
 Length = 414

Score = 33.3 bits (71), Expect = 4.0
 Identities = 16/27 (59%), Positives = 17/27 (62%), Gaps = 7/27 (25%)

Query: 5 GHPLLLGLLLV--LGPSPEQRVEIVPR 29
 G LLL LLLV LGP+ EQ VPR
 Sbjct: 292 GQSLLLFLLLVLTGLGA-EQ----VPR 313

☐ >[gi|13569709|gb|AAK31204.1|](#) bilirubin UDP-glucuronosyltransferase 1-1 [Homo sapien
 Length = 66

Score = 32.5 bits (69), Expect = 7.2
 Identities = 12/15 (80%), Positives = 13/15 (86%), Gaps = 1/15 (6%)

Query: 5 GHPLLLGLLL-VLGP 18
 G PL+LGLLL VLGP
 Sbjct: 8 GRPLVLGLLLCVLGP 22

☐ >[gi|8850236|ref|NP_000454.1|](#) ☒ UDP glycosyltransferase 1 family, polypeptide A1
 bilirubin UDP-glucuronosyltransferase isozyme 1 [Homo
 sapiens]

[gi|136729|sp|P22309|UD11_HUMAN](#) ☒ UDP-glucuronosyltransferase 1-1 precursor, micro
 (UDP-glucuronosyltransferase 1A1) (UDPGT) (UGT1*1)
 (UGT1-01) (UGT1.1) (UGT-1A) (UGT1A) (Bilirubin specific
 UDPGT isozyme 1) (HUG-BR1)

[gi|87534|pir||A39092](#) glucuronosyltransferase (EC 2.4.1.17) 1 precursor,
 bilirubin-specific - human

[gi|184473|gb|AAA63195.1|](#) ☒ UDP-glucuronosyltransferase 1

[gi|6094671|gb|AAF03522.1|](#) ☒ UDP-glucuronosyltransferase 1 [Homo sapiens]

[gi|11118749|gb|AAG30424.1|](#) UDP glucuronosyltransferase 1A1 [Homo sapiens]

[gi|40849850|gb|AAR95637.1|](#) ☒ UDP glycosyltransferase 1 family polypeptide A1 [Hom
[gi|742224|prf||2009308A](#) bilirubin UDP glucuronosyltransferase:ISOTYPE=1

Length = 533

Score = 32.5 bits (69), Expect = 7.2

Identities = 12/15 (80%), Positives = 13/15 (86%), Gaps = 1/15 (6%)

Query: 5 GHPLLLGLLL-VLGP 18

G PL+LGLLL VLGP

Sbjct: 8 GRPLVLGLLLCVLGP 22

☐ >[gi|45199011|ref|NP_986040.1|](#) AFR493Cp [Eremothecium gossypii]

[gi|44985086|gb|AAS53864.1|](#) AFR493Cp [Eremothecium gossypii]

Length = 324

Score = 32.5 bits (69), Expect = 7.2

Identities = 13/19 (68%), Positives = 13/19 (68%), Gaps = 6/19 (31%)

Query: 24 VEIVPRD---LRMKDKFLK 39

VEIVPRD L M KFLK

Sbjct: 42 VEIVPRDSPHL-M--KFLK 57

☐ >[gi|3059177|dbj|BAA25600.1|](#) bilirubin UDP-glucuronosyltransferase 1 [Homo sapien

Length = 50

Score = 32.5 bits (69), Expect = 7.2

Identities = 12/15 (80%), Positives = 13/15 (86%), Gaps = 1/15 (6%)

Query: 5 GHPLLLGLLL-VLGP 18

G PL+LGLLL VLGP

Sbjct: 8 GRPLVLGLLLCVLGP 22

☐ >[gi|6456550|gb|AAF09177.1|](#) UDP-glucuronosyltransferase 1A1 [Pongo pygmaeus]

Length = 27

Score = 32.5 bits (69), Expect = 7.2

Identities = 12/15 (80%), Positives = 13/15 (86%), Gaps = 1/15 (6%)

Query: 5 GHPLLLGLLL-VLGP 18

G PL+LGLLL VLGP

Sbjct: 8 GRPLVLGLLLCVLGP 22

☐ >[gi|38106605|gb|EAA52893.1|](#) hypothetical protein MG06021.4 [Magnaporthe grisea 7

Length = 419

Score = 32.5 bits (69), Expect = 7.2

Identities = 18/33 (54%), Positives = 21/33 (63%), Gaps = 6/33 (18%)

Query: 13 LLVLGPSPEQRVEIVPR--DLRMKDKF-LKHLT 42

LLVL PS QR IV R LR++D F L +LT

Sbjct: 170 LLVLSPS--QRAAIVARLSVLRIRD-FMLPNLT 199